

# SEQUENCE LISTING

<110> MEEK, THOMAS  
 PATEL, MEHUL  
 THRALL, SARA D.

<120> METHODS OF AND COMPOUNDS FOR MODULATING  
 THE ACTIVITY OF BACTERIAL FabG

<130> P51217

<140> TO BE ASSIGNED

<141> 2001-12-19

<150> 60/259,595

<151> 2000-01-03

<160> 2

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 243

<212> PRT

<213> Streptococcus pneumoniae

<400> 1

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Ile Gly Leu Ala Ile Ala His Lys Phe Ala Gln Ala Gly Ala Asn Ile
      20             25             30
Val Leu Asn Ser Arg Gly Ala Ile Ser Glu Glu Leu Leu Ala Glu Phe
      35             40             45
Ser Asn Tyr Gly Ile Lys Val Val Pro Ile Ser Gly Asp Val Ser Asp
      50             55             60
Phe Ala Asp Ala Lys Arg Met Ile Asp Gln Ala Ile Ala Glu Leu Gly
65             70             75             80
```

Ser Val Asp Val Leu Val Asn Asn Ala Gly Ile Thr Gln Asp Thr Leu  
 85 90 95  
 Met Leu Lys Met Thr Glu Ala Asp Phe Glu Lys Val Leu Lys Val Asn  
 100 105 110  
 Leu Thr Gly Ala Phe Asn Met Thr Gln Ser Val Leu Lys Pro Met Met  
 115 120 125  
 Lys Ala Arg Glu Gly Ala Ile Ile Asn Met Ser Ser Val Val Gly Leu  
 130 135 140  
 Met Gly Asn Ile Gly Gln Ala Asn Tyr Ala Ala Ser Lys Ala Gly Leu  
 145 150 155 160  
 Ile Gly Phe Thr Lys Ser Val Ala Arg Glu Val Ala Ser Arg Asn Ile  
 165 170 175  
 Arg Val Asn Val Ile Ala Pro Gly Met Ile Glu Ser Asp Met Thr Ala  
 180 185 190  
 Ile Leu Ser Asp Lys Ile Lys Glu Ala Thr Leu Ala Gln Ile Pro Met  
 195 200 205  
 Lys Glu Phe Gly Gln Ala Glu Gln Val Ala Asp Leu Thr Val Phe Leu  
 210 215 220  
 Ala Gly Gln Asp Tyr Leu Thr Gly Gln Val Ile Ala Ile Asp Gly Gly  
 225 230 235 240  
 Leu Ser Met

<210> 2

<211> 732

<212> DNA

<213> Streptococcus pneumoniae

<400> 2

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 tcagaagaat tgctcgctga gttttcaaac tatgggtatca aggtgggttcc catttcagga 180  
 gatgtatcag attttgcaga cgctaagcgt atgattgatc aagctattgc agaactgggt 240  
 tcagtagatg ttttgggtcaa caatgcaggg attacccaag atactcttat gctcaagatg 300  
 acagaagcag attttgaaaa agtgctcaag gtcaatctga ctgggtgcctt taatatgaca 360  
 caatcagtct tgaaaccgat gatgaaagcc agagaaggtg ctatcattaa tatgtctagt 420  
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gctacactag ctcagattcc gatgaaagaa tttgggcagg cagagcaggt tgcagatttg 660  
acagtatttt tagcaggcca agattatcta actggtcaag tgattgccat tgatggtggc 720  
ttaagtatgt ag 732

gctacactag ctcagattcc gatgaaagaa tttgggcagg cagagcaggt tgcagatttg 660  
acagtatttt tagcaggcca agattatcta actggtcaag tgattgccat tgatggtggc 720  
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